CEBS goals

A high quality public knowledgebase that aims to:

- **Create a reference toxicogenomic information system of studies on environmental chemicals and stressors and their effects (a public resource for the scientific community).**

- **Develop relational and descriptive data compendia on toxicologically important genes, groups of genes, SNPs, mutants and their attributes across species that are relevant to human health and environmental disease.**

- **Support hypothesis-driven and discovery research in environmental toxicology - and the research needs of risk assessment.**

- **Create a vehicle for the evolution of "systems toxicology".**

- **Identify molecular pathways leading to disease**

- **Improve ability to extrapolate from animal studies to probable human effects**

- **Provide better understanding of gene-environment interactions in human disease**

CEBS short-term plans: launch 4Q05

NCT National Center *for* Toxicogenomics

BIOINFORMATICS *to* **KNOWLEDGE**

Welcome to the National Institute of Environmental Sciences (NIEHS) National Center for Toxicogenomics (NCT) Chemical Effects in Biological Systems (CEBS) knowledgebase.

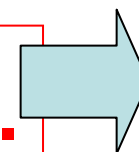* Query / Filter CEBS to Select Data of Interest:
- First by **Study Characteristics**
  e.g. select by stressor type, summary phenotype, species, key words, etc.
- First by **Individual Subject Characteristics**
  e.g. select by toxicity endpoint, other characteristics of the subject

* Display / Analyze Data in CEBS:
- Display **All** Investigations/Studies currently in CEBS
- Analyze **Microarray** (go directly to the microarray data without selecting first)
- Browse **Proteomics** (go directly to the microarray data without selecting first)

You can use any or all these ways to reach the data in CEBS. View all the data, or use the filters to select studies or individual subjects of interest. Once you have selected, you can continue filtering or view / analyze the data associated with the subjects you have selected.

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CHEMICAL EFFECTS *in* BIOLOGICAL SYSTEMS

Home

CEBS 1.4.1 Released!

Microarray

Proteomics

Systox

SysBio OM

Click on **Microarray** to access the CEBS Microarray Site

Click on **Proteomics** to access the CEBS Proteomics Site (Under Construction)

Welcome to the National Institute of Environmental Sciences (NIEHS) National Center for Toxicogenomics (NCT) Chemical Ef base. The knowledge base is still a work in progress but as we move forward, more and more features will be available to the

The NIEHS and NCT are working to help the field of environmental health research evolve into a knowledge-based science in v and informatics tools will play a significant role in improving our understanding of toxicant-related disease. The Chemical Effe for high quality data that is publicly accessible in a relational database that is compatible with standard laboratory output plat strategic toxicogenomics experimental design and conduct. Standardized procedures, protocols, data formats, and assessm uniform high level of quality. Raw data sets from NCT experiments will be available in their entirety.

and mutant ure and sto l guide res

CEBS will be linked extensively to other databases and to web genomics and proteomics resources, providing users the suit toxicogenomics data.

Future promises of CEBS include:

- Developing large context-annotated datasets that allow precise definition of biological/toxicological pa biomarkers.
- Linking genomic sequence to expression data to determine those genes that may be responsible for
- Increasing the interpretability and dimensionality of expression data by including data from new types
- Aiding in development of new algorithms and computational tools that allow predictive modeling of ge
- The CEBS knowledge base will support research that promotes mechanistic understanding of enviror mechanistic knowledge will make predictive toxicology possible and improve exposure assessment a
- The ultimate goal of the NCT, therefore, is to create a knowledgebase that allows environmental healt prevent adverse environmental exposure in the 21st century.

CEBS will store data from both microarray and proteomics experiments (see the labeled buttons above - currently only the Mi The database is designed to hold data that is public (that which has been published or released by the submitting investigato published or released). At this time, there is no publicly accessible data available.

- **http://cebs.niehs.nih.gov/**

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Microarray Home

~~Submit Experiment~~

Search and Analyze

~~Documentation Center~~

CEBS Microarray Home

From this page, you can submit microarray data and experiment information, or search and analyze existing tox

Submit Microarray Data and Experiment Information

Contribute your toxicogenomics microarray experiments here and join our community of contributing scientists.

Step-by-step instructions for experiment submissions that encompass all MIAME aspects, including processed a for download or on-line viewing.

Please select one of the following options:

Tutorial: View a Detailed Tutorial regarding experiment submissions to CEBS.

Prerequisites: View step-by-step prerequisites and required data for an experiment submis

Submit Experiment: For experienced users, go directly to Experiment Submission. (Requires Log

Restart Submission: Restart a previous, partially completed experiment submission. (Requires Lc

Add/Replace Hybridizations: Add or replace hybridizations associated with an experiment. (Requires Logi

Other MIAME Data: Submit Chip Design, Hardware, Software, or Protocol descriptions.

Search and Analyze Microarray Data

Search and analyze toxicogenomics microarray experiments submitted by fellow scientists. You may either dow toxicogenomics microarray experiments with a growing set of microarray analysis features in CEBS.

The Following Features are Available:

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Microarray Home
Submit Experiment
Search and Analyze
Documentation Center

Microarray Data Analysis Options

Welcome to CEBS Microarray Analysis page! CEBS provides an integrated solution for viewing and ana platforms. Currently, the following major functionalities are supported by CEBS Analysis Tools:

- Data Preprocessing
- Data Comparison
- Data Visualization
- Identification of Differentially Expressed Genes
- Gene Category Analysis by BioCarta Pathways
- Gene Category Analysis by KEGG Pathways
- Gene Category Analysis by Gene Ontology (GO)

To begin data viewing & analysis with these tools, please select experimental data first:

Search Experiment(s) for Analysis

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Documentation Center

Experiment Search

Experiment ID	
Investigator's Name	All
Experiment Title	All
Tissue Name	All
Species	All
Image Processing Software	All Microarray

> **Search Experiments**

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List of Experiments for Selection

Microarray Home
Submit Experiment
Search and Analyze
Documentation Center

The experiment search returns 4 record(s)

Please use check boxes below to select experiment(s), then click on "View Details about Selected Experiment(s)" for Analysis as well

important!

Select	Experiment ID	Investigator	Experiment Title	Image Processing Software
☐	482465666	Alexandra Heinloth	Gene Expression Profiling of F344/N Rat Livers After Acute Acetaminophen Exposure	Agilent
☐	544	Alexandra Heinloth	Gene Expression Profiling of F344/N Rat Livers After Acute Acetaminophen Exposure	Affymetrix
☐	525058561	Robert Williams	Mouse QTL strains - hematopoetic stem cells	Affymetrix
☐	527402005	Robert Williams	Mouse QTL strains - forebrain	Affymetrix

> **Reset**

> **View Details about Selected Experiment(s)**

To learn about the data

Brief View

- Click on "Experiment ID" to view experiment information report in the **Detailed View**.
- For analysis, use the check box below to select experiment(s), then click on "Analyze Selected Experiment(s)".
- Multiple experiments can be analyzed together, if they have same platform & matched array design (ID).

Analyze	Experiment ID	Investigator	Experiment Title	Image P Soft
☐	482465666	Alexandra Heinloth	Gene Expression Profiling of F344/N Rat Livers After Acute Acetaminophen Exposure	Agilent
☐	522398544	Alexandra Heinloth	Gene Expression Profiling of F344/N Rat Livers After Acute Acetaminophen Exposure	Affymetrix

important!

Analyze Selected Experiment(s)

Detailed View

Gene Expression Profiling of F344/N Rat Livers After Acute Acetaminophen

Experiment ID	482465666
Investigator Name	Alexandra Heinloth
Organization	NCT
Experiment Type	Treatment vs. Untreated Comparison
Species	[Rat]
Tissue(s)	[Liver left lateral lobe]
Image Processing Software	Agilent
Array Design Name	Rat Oligo Microarray
Array Design ID	274252003
Stressor Name(s)	Acetaminophen
Experimental Variable(s)	Acetaminophen (Dose Level,Time)
Characteristics That Vary Between Samples	None
Publication	
Submission Date	2004-11-15

Select Arrays for Analysis

Gene Expression Profiling of F344/N Rat Livers After Acute Acetaminophen Exposure

Experiment 1 of 1

Select All	None	Array Name	Sample Name	Dose Level	Time
☑	1500mg_Acetaminophen_24h_Male_Rat_3018_206559593	1500mg_APAP_24hr_3018	1500 mg/kg	24 hour
☑	1500mg_Acetaminophen_24h_Male_Rat_3019_206559594	1500mg_APAP_24hr_3019	1500 mg/kg	24 hour
	...hen_24h_Male_Rat_3020_206559595	1500mg_APAP_24hr_3020	1500 mg/kg	24 hour
☑	...hen_24h_Male_Rat_Pool_206771750	1500mg_APAP_24hr_Pool_3012_3013_3014	0 mg/kg	24 hour
☐	1500mg_Acetaminophen_48h_Male_Rat_3006_206559596	1500mg_APAP_48hr_3006	1500 mg/kg	48 hour
☐	1500mg_Acetaminophen_48h_Male_Rat_3007_206559597	1500mg_APAP_48hr_3007	1500 mg/kg	48 hour
☐	1500mg_Acetaminophen_48h_Male_Rat_3008_206559598	1500mg_APAP_48hr_3008	1500 mg/kg	48 hour
☑	1500mg_Acetaminophen_48h_Male_Rat_Pool_206559665	1500mg_APAP_48hr_Pool_3000_3001_3002	0 mg/kg	48 hour
☐	1500mg_Acetaminophen_6h_Male_Rat_3030_206559590	1500mg_APAP_6hr_3030	1500 mg/kg	6 hour
☐	1500mg_Acetaminophen_6h_Male_Rat_3031_206559591	1500mg_APAP_6hr_3031	1500 mg/kg	6 hour
☐	1500mg_Acetaminophen_6h_Male_Rat_3032_206559592	1500mg_APAP_6hr_3032	1500 mg/kg	6 hour
☐	150mg_Acetaminophen_24h_Male_Rat_3069_206266694	150mg_APAP_24hr_3069	150 mg/kg	24 hour
☐	150mg_Acetaminophen_24h_Male_Rat_3070_206266695	150mg_APAP_24hr_3070	150 mg/kg	24 hour
☐	150mg_Acetaminophen_24h_Male_Rat_3074_206266696	150mg_APAP_24hr_3074	150 mg/kg	24 hour
☑	150mg_Acetaminophen_24h_Male_Rat_Pool_206771749	150mg_APAP_24hr_Pool_3064_3065_3067	0 mg/kg	24 hour
☐	150mg_Acetaminophen_48h_Male_Rat_3057_206559587	150mg_APAP_48hr_3057	150 mg/kg	48 hour
☐	50mg_Acetaminophen_6h_Male_Rat_3126_206559579	50mg_APAP_6hr_3126	50 mg/kg	6 hour
☐	50mg_Acetaminophen_6h_Male_Rat_3127_206559580	50mg_APAP_6hr_3127	50 mg/kg	6 hour
☐	50mg_Acetaminophen_6h_Male_Rat_Pool_206559657	50mg_APAP_6hr_Pool_3131_3132_3133	0 mg/kg	6 hour

important!

< Back   > Continue

Data Set Preprocessing Options

Spot Filtering

Intensity Threshold:	20
Consider Intensity under Threshold as:	Threshold
Filter by Absolute Call:	Include all probe sets
Consider Excluded Probe Sets as:	Missing Value

Scaling/Normalization

|	
Scale/Normalize by:	Mean intensity of all probe sets
Trim:	0.02
Target Intensity:	500
☐ Perform Cross-array Normalization Based on:	Inter-quartile range

Back   Continue

Microarray Data Analysis Options

A processed data set has been generated.   It is stored at the server and ready for further analyses.

You are now ready to continue microarray analysis on the preprocessed data by clicking "Analyze Preprocessed Data". Alternatively, you may choose to view the exploratory plots of the preprocessed data before you go ahead for further analysis, by clicking "Visualize Preprocessed Data".

Analyze Preprocessed Data
Visualize Preprocessed Data

Box-Whisker Plot

This plot displays distribution characteristics, such as central tendency (median) and ranges (the lower and upper quartiles) of data from each array. The log scale is used.
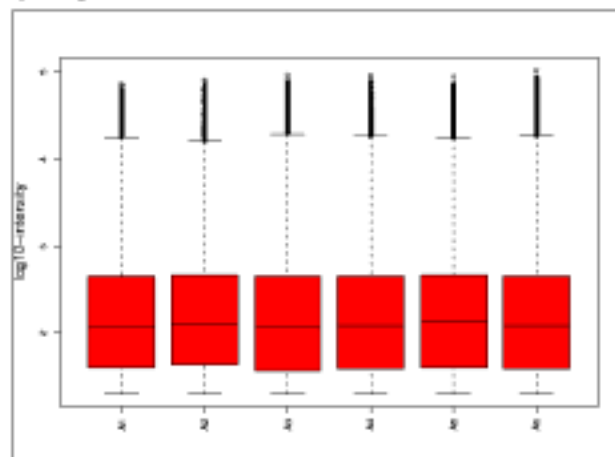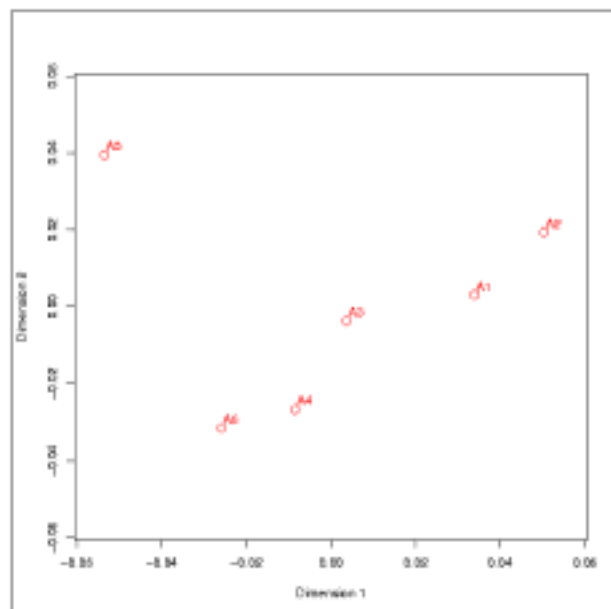

See Legend for Array Information
Back to Preprocessing | Continue Microarray Analysis

Multi-dimensional Scaling Plot

This plot displays the relative similarities of arrays (and the gene expression of samples therein) by projecting the distances between arrays (based on 1-pearson correlation) from high dimensional into two-dimensional space using multi-dimensional scaling algorithm.

See Legend for Array Information
Back to Preprocessing | Continue Microarray Analysis
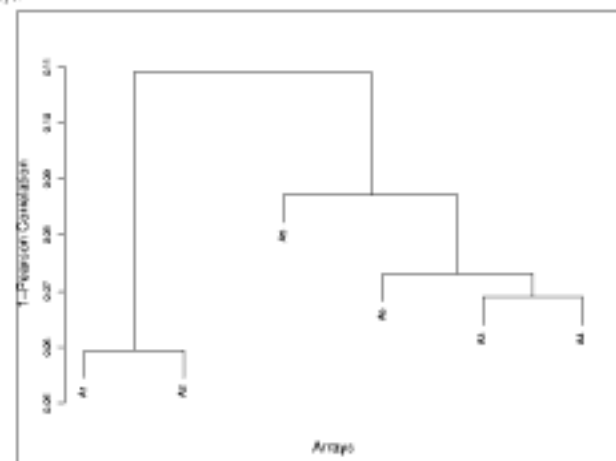
Legend for Array Information

Label	Experiment ID	Array Name	Sample Name
A1	522388544	1500mg_Acetaminophen_24h_Male_Rat_3019_206559591	1500mg_APAP_24hr_3019
A2	522388544	1500mg_Acetaminophen_24h_Male_Rat_3019_206559594	1500mg_APAP_24hr_3019
A3	522388544	1500mg_Acetaminophen_24h_Male_Rat_3020_206559595	1500mg_APAP_24hr_3020
A4	522388544	1500mg_Acetaminophen_24h_Male_Rat_Pool_206771750	1500mg_APAP_24hr_Pool_3012_3013_3014
A5	522388544	1500mg_Acetaminophen_48h_Male_Rat_Pool_206559565	1500mg_APAP_48hr_Pool_3000_3001_3002
A6	522388544	150mg_Acetaminophen_24h_Male_Rat_Pool_206771748	150mg_APAP_24hr_Pool_3064_3065_3067

Experiment Information

Experiment ID	Title
522388544	Gene Expression Profiling of F344/N Rat Livers After Acute Acetaminophen Exposure

Clustering of Arrays

This plot displays the relative similarities between arrays (based on Pearson correlation of global expression), and hierarchical clustering of arrays.

See Legend for Array Information
Back to Preprocessing | Continue Microarray Analysis

Perform Comparison Analysis to Identify Differentially Expressed Genes

Differentially expressed genes are identified by magnitude and statistical significance (when applicable) of the difference. CEBS provides several statistical tests, as well as means to control False Discovery Rate (FDR) and Family-wise Error Rate (FWER) for comparison analysis.

○ **Comparison of Two Groups of Arrays:** The comparison will be performed between the expression values (i.e. intensities or ratio, possibly with log transformation) of different groups of arrays. This type of comparison can be used with Affymetrix GeneChip data, two-channel array data with common reference, or whenever it is appropriate to compare the ratios between groups of arrays.

○ **Comparison of Samples in the Same Arrays:** This type of comparison is based on the deviation of the ratios (of intensities between two channels) from 1, or log-ratios from 0. The statistical significance will be based on variance of expression values for each gene across replicate arrays. No cross-gene error model is used in current implementation.

‹ Back   › Continue

Select Arrays for Comparison Analysis

Please select arrays that you wish to compare, either *with* or *without* replicates. If there are replicates for both conditions, statistical significance will be evaluated using the methods on the next page.

Experiment	Array Name	Sample Name	Array Group A	Array Group B	Neither
522398544	1500mg_Acetaminophen_24h_Male_Rat_3018_206559593	1500mg_APAP_24hr_3018	●	○	○
522398544	1500mg_Acetaminophen_24h_Male_Rat_3019_206559594	1500mg_APAP_24hr_3019	●	○	○
522398544	1500mg_Acetaminophen_24h_Male_Rat_3020_206559595	1500mg_APAP_24hr_3020	●	○	○
522398544	1500mg_Acetaminophen_24h_Male_Rat_Pool_206771750	1500mg_APAP_24hr_Pool_3012_3013_3014	○	●	○
522398544	1500mg_Acetaminophen_48h_Male_Rat_Pool_206559665	1500mg_APAP_48hr_Pool_3000_3001_3002	○	○	●
522398544	150mg_Acetaminophen_24h_Male_Rat_Pool_206771749	150mg_APAP_24hr_Pool_3064_3065_3067	○	●	○

< Back   > Continue   > Reset

Define Criteria for Differentially Expressed Gene(s)

>> Minimum Fold Change: 2

>> Statistical Significance: (only applicable when comparing multiple samples/arrays)

Step 1. Choose the following test for each gene:

- ⦿ t test: Welch's two sample t test
- ○ Wilcoxon test: Mann-Whitney test

Step 2. Choose a *p*-value threshold and a multiple testing procedure to apply:

- ⦿ Directly use single gene test *p*-values at threshold of [0.05 ▼]
- ○ Control False Discovery Rate (*FDR*) with adjusted *p*-value below [0.1 ▼]
  Method to control *FDR*:
    - ⦿ Benjamini & Hochberg step-up procedure
    - ○ Benjamini & Yekutieli step-up procedure
- ○ Control Family-wise Type-I Error Rate (*FWER*) with adjusted *p*-value below [0.1 ▼]
  Method to control *FWER*:
    - ⦿ Holm step-down procedure
    - ○ Sidak single-step procedure
    - ○ Sidak step-down procedure
    - ○ Bonferroni
- ○ Do not use the *p*-values for gene selection

◁ Back   ▷ Submit   ▷ Reset

Biological Analysis of Gene Expression Data

Biological analyses are performed on the result of previous statistical analysis, e.g. the comparison analysis. Biological annotation and information about categories of biological activities (CBA) from different sources are incorporated during this stage of analysis to facilitate understanding of gene expression data.

⊙ **View Expression Report for All Differentially Expressed Genes**

○ **Perform Gene Category Analysis by BioCarta Pathways**

○ **Perform Gene Category Analysis by KEGG Pathways**

○ **Perform Gene Category Analysis by Gene Ontology (GO)**

Disclaimer: Academicians and non-academicians must refer to BioCarta Terms and Conditions and KEGG Terms and Conditions for additional use of this material.

‹ **Back**   › **Continue**

All Differentially Expressed Genes

- Total Number of Differentially Expressed Genes: 917
- This Table is Sortable by Clicking on a Column Header

Records 1 - 200   Page 1 of 5 ▶   Go to Page 1

Probe set	Gene Symbol	Gene Title	Mean log2 intensity of group A	Mean log2 intensity of group B	Change	log2(A)-log2(B)	A/B	Raw p-value
1389612_at	Unnamed Gene	Transcribed locus, moderately similar to NP_001001306.1 hypothetical protein D030034H09 [Mus musculus]	9.88886	11.38244	Down	-1.49358	0.35513	0.04349
1389384_at	*BE111733	NA	11.22106	10.15727	Up	1.06379	2.09042	0.04211
1389430_at	Unnamed Gene	Transcribed locus	8.96998	10.32433	Down	-1.35435	0.39111	0.00708
1389437_at	Unnamed Gene	Similar to Sal-like protein 2 (Spalt-like protein 2) (MSal-2)	5.94028	4.32193	Up	1.61835	3.07025	0.00864
1389502_at	Unnamed Gene	Transcribed locus	6.57272	4.43464	Up	2.13808	4.40176	0.00234
1389510_at	Unnamed Gene	Transcribed locus	9.90972	8.88868	Up	1.02105	2.02939	0.00042
1389511_s_at	*BF403383	NA	8.70085	9.73153	Down	-1.03068	0.48948	0.02693
1389232_at	LOC60380	Growth and transformation-dependent protein	6.86591	5.70581	Up	1.16010	2.23473	0.04147
1389279_at	Unnamed Gene	Similar to N-acetylglucosaminyltrasnferase Mb	9.50065	8.12528	Up	1.37537	2.59434	0.01938
1389048_at	Unnamed Gene	Transcribed locus, strongly similar to NP_033885.2 bone morphogenetic protein 1 [Mus musculus]	8.73004	9.97310	Down	-1.24307	0.42247	0.02287
1389055_at	Unnamed Gene	Transcribed locus	9.32839	8.13943	Up	1.18897	2.27989	0.04478
1389094_at	*BI297318	NA	6.42570	4.33601	Up	2.08969	4.25655	0.02333
1389111_at	Unnamed Gene	Transcribed locus	10.54704	12.09545	Down	-1.54841	0.34189	0.00817
1388873_at	Idi1	...pentenyl-diphosphate delta isomerase	8.35885	10.69134	Down	-2.33249	0.19854	0.04999
1388898_at	Unnamed Gene	Similar to heat shock protein 105 kDa alpha	13.42131	11.84942	Up	1.57189	2.97294	0.01557
1388909_at	Unnamed Gene	Similar to cDNA sequence BC019806	10.17703	9.05765	Up	1.11938	2.17254	0.00282
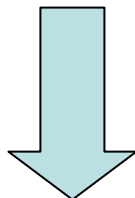
annotation (next page)

Gene Info Page

Gene Information For: Rn Idi1 isopentenyl-diphosphate delta isomerase

Sequence ID: NM_053539

Database Links

UniGene LocusLink   DTP SNPViewer Assemblies SNPs SNP500Cancer

Libraries and Tissues (from EST Data)

- This gene is found in these libraries

- Monochromatic SAGE/cDNA Virtual Northern

Protein Similarities (from UniGene)

Organism	Protein ID	% Similarity	Aligned aa
Rn	ref NP_445991 1	100	227
Mm	sp P58044	92	227
Hs	ref NP_004499 1	86	227
Ce	pir S44843	38	224
Ec	ref NP_289458 1	29	147
At	ref NP_186927 1	49	227
null	pir A34440	49	221

Orthologs (from HomoloGene)

Symbol	Name	Sequence	CGAP Gene Info	Reference	% Similarity
IDI1	Isopentenyl-diphosphate delta isomerase	NM_004508	Gene Info	-	84.1
Idi1	Isopentenyl-diphosphate delta isomerase	NM_177960 NM_145360	Gene Info	-	92.8
3J183	Isopentenyl-diphosphate delta-isomerase (3J183)	NM_066365	Gene Info	-	50.3

Gene Ontology

Human Classification by Proteome, as Recorded In LocusLink   Mouse classification by The Jackson Laboratory, as recorded in LocusLink

- magnesium ion binding

Gene Categories Represented in Array

Category information Provided by BioCarta (See Terms and Conditions of use)

- Total Number of Gene Categories: 376
- View Differentially Expressed Genes Not In Any BioCarta Pathways
- This Table is Sortable by Clicking on a Column Header

SORT

VIEW

Gene Category Name	Total	Down	Change	Enrichment	Fisher Exact Test p-value	View Detailed Expression Reports
Tumor Suppressor Arf Inhibits Ribosomal Biogenesis	12				0.00401	Genes|Diagram
Sumoylation by RanBP2 Regulates Transcriptional Repression	14	3	8	3	7.26615	8.8873	Genes|Diagram
ADP-Ribosylation Factor	20	8	3	2	5.08551	0.02895	Genes|Diagram
IL12 and Stat4 Dependent Signaling Pathway in Th1 Development	22	1	3	3	4.62339	8.02594	Genes
CTCF: First Multivalent Nuclear Factor	26	3	8	3	3.872	0.0481T	Genes
Eicosanoid Metabolism	27	2	1	3	3.76711	0.04423	Genes
SREBP control of lipid synthesis	12	8	3	2	5.85887	0.04715	Genes|Diagram
Map Kinase Inactivation of SMRT Corepressor	13	9	3	2	5.21801	0.05496	Genes|Diagram
p38 MAPK Signaling Pathway	32	1	3	3	3.1795	8.887A	Genes|Diagram
Neuroregulin receptor degradation protein-1 Controls ErbB3 receptor recycling	15	1	1	3	4.52854	8.8788	Genes
Role of EGF Receptor Transactivation by GPCRs in Cardiac Hypertrophy	15	1	1	2	4.52854	8.8788	Genes|Diagram
EGF Signaling Pathway	34	1	3	3	2.98193	0.07793	Genes|Diagram
The role of FYVE-finger proteins in vesicle transport	3	8	1	1	11.20134	8.8859	Genes|Diagram
Cycling of Ran in nucleocytoplasmic transport	4	1	8	1	8.47801	0.11297	Genes|Diagram
Cell Cycle: G2/M Checkpoint	20	2	8	3	3.3884	0.11840	Genes|Diagram
ATM Signaling Pathway	21	2	8	2	3.22895	0.12833	Genes|Diagram
Rac 1 cell motility signaling pathway	21	8	3	2	2.22896	0.13833	Genes|Diagram
Degradation of the RAR and RXR by the proteasome	5	1	8	1	6.76801	0.13934	Genes|Diagram

Gene Category: Tumor Suppressor Arf Inhibits Ribosomal Biogenesis

- Total Number of Records: 12
- *This Table is Sortable by Clicking on a Column Header*

Probe set	Gene Symbol	Gene Title	Mean log2 intensity of group A	Mean log2 intensity of group B	Change	log2(A): log2(B)	A/B	Raw p-value
1387750_at	Twist	Twist gene homolog, (Drosophila)	4.32193	4.32193	Unchanged	0.00000	1.00000	NA
1384427_at	Unnamed Gene	Similar to mdm2 gene product	9.95960	8.87617	Up	1.08344	2.11908	0.03103
1375281_at	Tbx2	T-box 2	7.40575	6.29300	Unchanged	1.11276	2.16259	0.52968
1383485_at	Unnamed Gene	Similar to mdm2 gene product	8.66816	7.69956	Unchanged	0.96860	1.95694	0.30605
1371713_at	Abl1	Abelson murine leukemia viral (v-abl) oncogene homolog 1	7.31093	7.62469	Unchanged	-0.31376	0.80454	0.64468
1395332_at	Tbx2	T-box 2	5.72483	5.57599	Unchanged	0.14884	1.10868	0.92563
1370752_a_at	Tp53	Tumor protein p53			Unchanged			
1368309_at	Myc	Myelocytomatosis viral oncogene homolog (avian)						
1367830_a_at	Tp53	Tumor protein p53						
1367831_at	Tp53	Tumor protein p53						
1383288_at	Unnamed Gene	Similar to mdm2 gene product						
1377702_at	Rb1	Retinoblastoma 1						
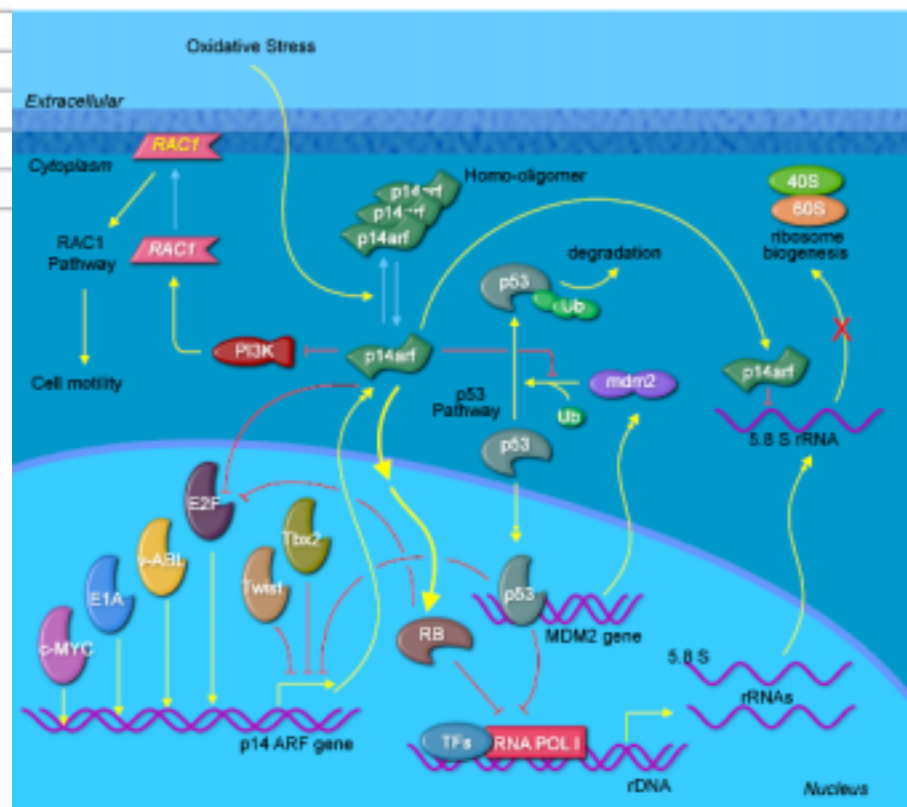
KEGG Pathway Analysis Reports

KEGG provides information about biological **pathways**, such as *Glycerolipid metabolism* and *Histidine metabolism*. Related KEGG pathways are organized together to represent more general **functional categories**, such as *Lipid Metabolism* and *Energy Metabolism*. CEBS utilizes KEGG pathway information to bin genes into categories of biological activities and evaluates gene expression at both individual pathway and the functional category levels.

⊙ **View Expression Report for KEGG Functional Categories**

   The *Expression Report for KEGG Functional Categories* provides overall gene expression information for each functional category. It also links to *Expression Report for Pathways* and *Genes* within each category.

○ **View Expression Report for KEGG Pathways**

   CEBS *Expression Report for Pathways* presents gene expression characteristics at the pathway level. Also provided are links to *Expression Report for Genes* within a given pathway and KEGG *Pathway Diagrams* (with differentially expressed genes highlighted in red).

< Back   > Continue
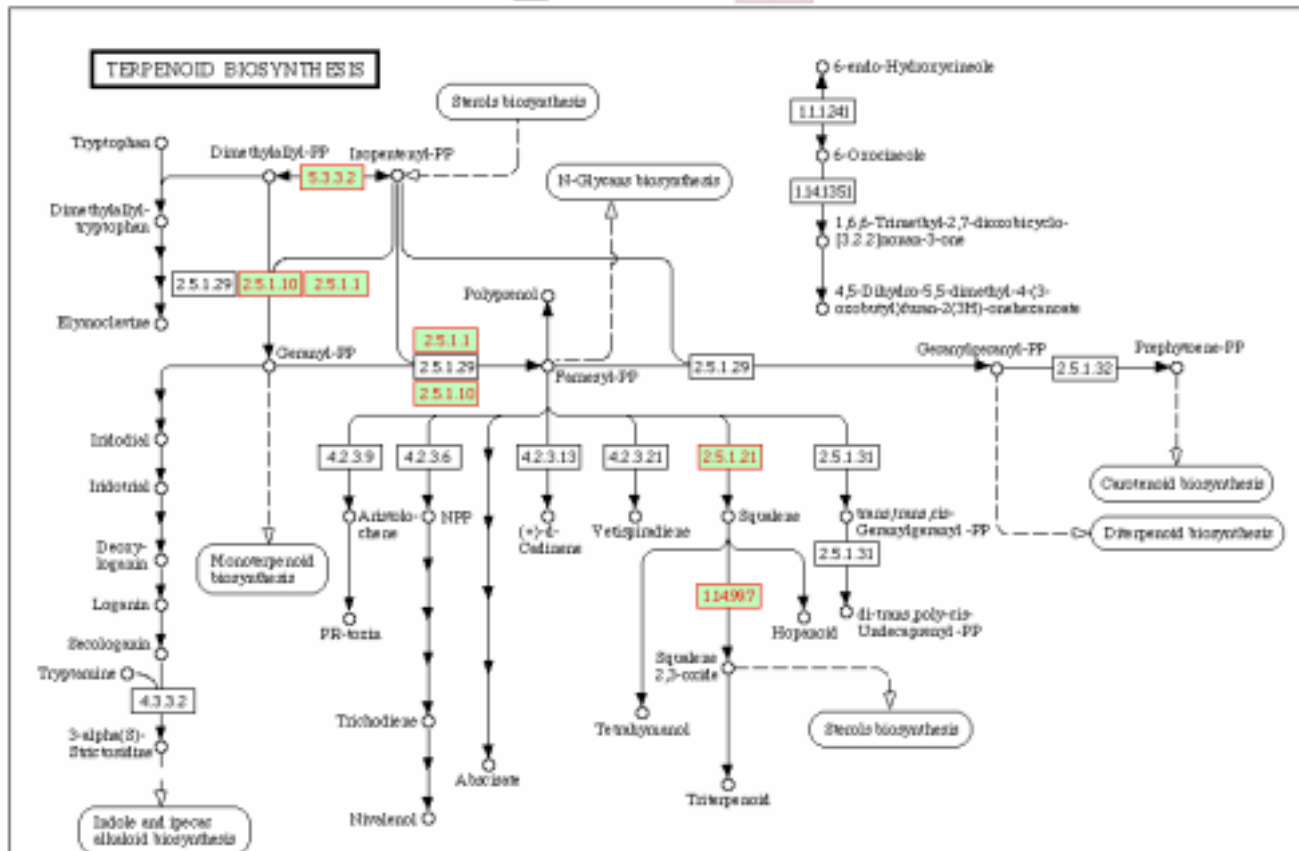
red outlines => changed transcripts

Gene Ontology Analysis Options

CEBS provides gene category analysis through Gene Ontology (GO), a controlled vocabulary built by The Gene Ontology Consortium.

GO defines three broad aspects of categories (*see below*). The children categories of these aspects represent lower levels of granularity with higher specificity.

Aspect Type	Definition
Biological Process	broad biological goals, such as ***mitosis*** or ***purine metabolism***, that are accomplished by ordered assemblies of molecular functions
Molecular Function	the tasks performed by individual gene products; examples are ***carbohydrate binding*** and ***ATPase activity***
Cellular Component	subcellular structures, locations, and macromolecular complexes; examples include ***nucleus***, ***telomere***, and ***origin recognition complex***

CEBS allows users to evaluate gene expression of GO categories at different granularity levels of a given aspect. Each GO category will be evaluated and ranked based on relative degree of change in gene expression. In addition to overall expression summary, detailed report of expression for genes in each GO category is also provided. Also provided are links to external GO resources for detailed GO annotation.

Select GO categories to be used in analysis:

Aspect Type   Granularity Level

Biological Process ▼   Level 3 ▼   Submit for Analysis

AmiGO

aging

Accession: GO:0007568
Aspect: biological_process
Synonyms:
GO:0016280
ageing
senescence
Definition:
The inherent decline over time, from the optimal fertility and viability of early maturity, that culminates in death and may be preceded by other indications, such

Term Lineage

all : all (216440)
  GO:0008150 : biological_process (143499)
    GO:0007275 : development (20087)
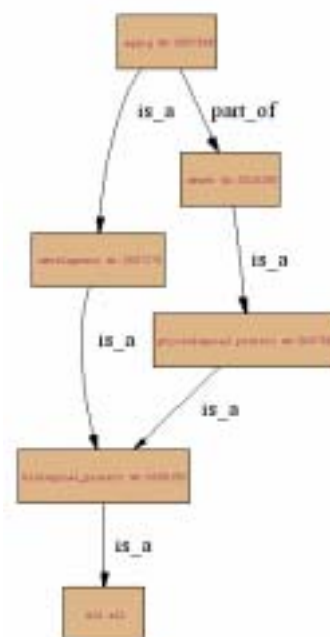   **GO:0007568 : aging (495)**
    GO:0007582 : physiological process (95002)
      GO:0016265 : death (2963)
        GO:0007568 : aging (495)

External References

TIGR_role (1)

Graphical View

Parent Categories:

| GO:0016265 | death | Gene Expression Report | AmiGO | QuickGO |
| GO:0007275 | development | Gene Expression Report | AmiGO | QuickGO |

Child Categories:

GO:0010149	senescence (sensu Magnoliophyta)	Gene Expression Report	AmiGO	QuickGO
GO:0042697	menopause	Gene Expression Report	AmiGO	QuickGO
GO:0008340	determination of adult life span	Gene Expression Report	AmiGO	QuickGO
GO:0007569	cell aging	Gene Expression Report	AmiGO	QuickGO

- Total Number of Records: 13
- *This Table is Sortable by Clicking on a Column Header*

Records 1 - 13

Probe set	Gene Symbol	Gene Title	Mean log2 intensity of group A	Mean log2 intensity of group B	Change	log2(A)- log2(B)	A/B	Raw p-value
1387531_at	Msra	Methionine sulfoxide reductase A	9.60532	10.30974	Unchanged	-0.70442	0.61369	0.10923
1370752_a_at	Tp53	Tumor protein p53	8.48752	8.25319	Unchanged	0.23432	1.17635	0.70505
1369361_at	Kl	Klotho	5.08470	4.32193	Unchanged	0.76277	1.69675	0.22829
1369194_a_at	Cdkn2a	Cyclin dependent kinase inhibitor 2A	4.32193	4.32193	Unchanged	0.00000	1.00000	NA
1368002_at	Msh2	Mismatch repair protein	7.88040	8.22442	Unchanged	-0.34401	0.78785	0.59029
1367830_a_at	Tp53	Tumor protein p53	9.16838	8.45984	Unchanged	0.70854	1.63415	0.47229
1367831_at	Tp53	Tumor protein p53	10.16190	9.60873	Unchanged	0.55318	1.46731	0.02607
1367609_at	Mif	Macrophage migration inhibitory factor	13.12239	12.18226	Unchanged	0.94013	1.91870	0.12077
1377527_at	Msra	Methionine sulfoxide reductase A	6.02496	6.44147	Unchanged	-0.41651	0.74923	0.69738
1398163_at	Msh2	Mismatch repair protein	4.32193	4.32193	Unchanged	0.00000	1.00000	NA
1399158_a_at	Npm1	Nucleophosmin 1	13.62844	12.28890	Up	1.33954	2.53070	0.03597
1398756_at	Npm1	Nucleophosmin 1	11.14738	9.46027	Up	1.68711	3.22012	0.01714
1398757_at	Npm1	Nucleophosmin 1	14.03840	12.67710	Up	1.36130	2.56917	0.01023

Related Information on Current Analysis: [Experiment/Array Selection ▼] [View]

CEBS is designed to be used both as a public resource and as a public-private resource.

Users can create a private area in CEBS, upload their data and then analyze their own data using CEBS tools, or select data already in CEBS on the same platform, and combine public and private data for analysis.

To set this up, please contact fostel@niehs.nih.gov

CEBS questions?
Interested in sharing your data in CEBS?

contact fostel@niehs.nih.gov